

**Nucleotide**

Alphabet of Life

**“Exhibit C”**

Display Settings: GenBank

**Porcine G protein gene, exon 1**

GenBank: M57287.1

FASTA Graphics

Features Sequence

LOCUS PIGI2AA 983 bp DNA linear MAM 27-APR-1993  
 DEFINITION Porcine G protein gene, exon 1.  
 ACCESSION M57287 4  
 VERSION M57287.1 GI:164496  
 KEYWORDS G protein.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.  
 REFERENCE 1 (bases 1 to 983)  
 AUTHORS Holtzman, E.J., Soper, B.W., Stow, J.L., Ausiello, D.A. and Ercolani, L.  
 TITLE Regulation of the G-protein alpha i-2 subunit gene in LLC-PK1 renal  
 cells and isolation of porcine genomic clones encoding the gene  
 promoter  
 JOURNAL J. Biol. Chem. 266 (3), 1763-1771 (1991) ←  
 PUBMED 1899094  
 FEATURES Location/Qualifiers  
 source 1..983  
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 /db\_xref="GI:164497"  
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 intron 713..>983  
 ORIGIN  
 1 atccccaaac aagtatttgg ggttcattaa cttaacaaa tgacgaagac acgcctcc  
 61 tactcatctc gctcgactct cagaagcttg gagggcttgt tccctgttgg cccgcggagg  
 121 gcaccggatc ctcatctcg ggctacgaga tccgcggcc cccggcgatc ggcagcggag  
 181 ctccaggcgcc tccgcaccca atcgagccc ggcccccgc tgcgtcaag cttctgtgct  
 241 aggctctacc cctacagcta tcccttggcg tggctccgcc ttcagccgc accgagttt  
 301 ggctgcgcct aacttctccc tcgagccat cactgacccc gggctctctg tggcccccgc  
 361 tccggcccg ccccgccca gtccctcgcc agactagctc gggcccccacc cccggcccg  
 421 cctgcgtcg gtgcgcggcg gcctggaaagg caccgcgtc agacgcgtgg aactgcggac  
 481 ccggagacta cccgttagagg gccggcgccg gcgggagccg agtgggtcg ggccggccga  
 541 gccggcccg ggccgtgtgg tggccggca gccggccggc cggccggacgg cggatgggc  
 601 tgcaccgtga ggcgtggaa caaggccggc gccgaggcgt cccaaatgtat cgacaagaac  
 661 ctgcggaaag acggcgagaa ggcggccgg gaggtgaagt tgctgtctt gggtgaggcc  
 721 ggcgtctcgctg ctgggacccc tgatcccata cccaaatgtat cttactttgac ctgcggacta  
 781 gtgttcgaa ctccccacact cggccgtggac ttaaccctgt agacccgcct ggcaaggaca  
 841 tacaaaataaa taatggatca aaactcaggg ttggccataga cctctcagat ccagagccca  
 901 gactcttagat cagactcaac tcatccccaa ccccgcccc ccaaaccagg acactgggtgc  
 961 ctcaacatcc gctgcccaga att

//

**BLAST****Basic Local Alignment Search Tool**

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Blast 2 sequences

**dbj|DD249890| (3871 letters)**Results for:  dbj|DD249890.1 Gm1 promoter and use thereof.(3871bp)

Your BLAST job specified more than one input sequence. This box lets you choose which input sequence to show BLAST results for.

**Query ID**gi|99025749|dbj|DD249890.1| ←  
gi|99025749|dbj|DD249890.1|**Description**

Gm1 promoter and use thereof.

**Molecule type**

dna

**Query Length**

3871

**Subject ID**

gi|164496|gb|M57287.1|PIGI2AA ←

**Description**

Porcine G protein gene, exon 1

**Molecule type**

nucleic acid

**Subject Length**

983

**Program**

BLASTN 2.2.24+ Citation

**Reference**

Zheng Zhang, Scott Schwartz, Lukas Wagner, and Webb Miller (2000), "A greedy algorithm for aligning DNA sequences", J Comput Biol 2000; 7(1-2):203-14.

⇒ • No significant similarity found. For reasons why, click here

Other reports: [Search Summary](#) [[Taxonomy reports](#)]**Search Parameters****Search parameter name** **Search parameter value**

Program blastn

NCBI Blast:dbj|DD249890| (3871 letters)

2/3 ページ

Word size 28  
 Expect value 10  
 Hitlist size 100  
 Match/Mismatch scores 1,-2  
 Gapcosts 0,0  
 Low Complexity Filter Yes  
 Filter string L;m;  
 Genetic Code 1

Karlin-Altschul statistics

**Params Ungapped Gapped**

Lambda	1.33271	1.28
K	0.620991	0.46
H	1.12409	0.85

Results Statistics

**Results Statistics parameter name Results Statistics parameter value**

Effective search space	3737433
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**Graphic Summary****Distribution of Blast Hits on the Query Sequence**

[?]

An overview of the database sequences aligned to the query sequence is shown. The score of each alignment is indicated by one of five different colors, which divides the range of scores into five groups. Multiple alignments on the same database sequence are connected by a striped line. Mousing over a hit sequence causes the definition and score to be shown in the window at the top, clicking on a hit sequence takes the user to the associated alignments. New: This graphic is an overview of database sequences aligned to the query sequence. Alignments are color-coded by score, within one of five score ranges. Multiple alignments on the same database sequence are connected by a dashed line. Mousing over an alignment shows the alignment definition and score in the box at the top. Clicking an alignment displays the alignment detail.

10/593,216 Gm1 promoter and use thereof

09-17-  
2010::10:01:28**Supplemental Content - Search Results**

This page gives you information about the number of versions associated with the application you requested. Use this page to obtain specific version information

Version Number	Item Id	Item Size
1	09323b6780c8016e	42.752
1	09323b6780c8016f	42.752
1	② 09323b6780c80170	42.752
1	09323b6780c80171	42.752
1	① 09323b6780c80172	42.752
1	09323b6780c80173	42.752
1	09323b6780c80174	42.752
1	09323b6780c80175	42.752
1	09323b6780c80176	42.752
1	09323b6780c80177	42.752
1	09323b6780c80178	42.752
1	09323b6780c80179	42.752

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